

us-08-711-417c-165.rng

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on:

August 28, 2002, 07:56:20 ; Search time 202.43 seconds
(without alignments)
13154.840 Million cell updates/sec

Title: US-08-711-417c-165

Perfect score: 1551

Sequence: 1 ATGCGATGCTGACGAGGTCAC.....ACCGCTCCACATGAGCTAA 1551

Scoring table: IDENTIFY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_032802:*

- 1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1980.DAT:*
- 2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT:*
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- 23: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
|------------|--------|-------|--------|----|-------------|
| 1 | 1551 | 100.0 | 1551 | 19 | AAV42840 |
| 2 | 1468.8 | 94.7 | 6439 | 21 | AAV42840 |
| 3 | 1386 | 89.4 | 1386 | 17 | AAV42840 |
| 4 | 1386 | 89.4 | 1386 | 19 | AAV42840 |
| 5 | 1382.4 | 89.1 | 1611 | 15 | AAQ44980 |
| 6 | 1379.6 | 88.9 | 1386 | 19 | AAV42806 |
| 7 | 1174.8 | 75.7 | 2049 | 17 | AAV42806 |
| 8 | 1174.8 | 75.7 | 2049 | 19 | AAV42806 |
| 9 | 1174.8 | 75.7 | 2049 | 19 | AAV42806 |

| | | | | | | |
|----|-------|------|------|----|----------|---------------------|
| 10 | 868 | 56.0 | 1004 | 17 | AAV42840 | Ikaro's cDNA. Not |
| 11 | 868 | 56.0 | 1004 | 19 | AAV42840 | Ikaro's isoform enc |
| 12 | 813.2 | 52.4 | 1788 | 15 | AAQ44979 | Human Ikaro's cDNA. |
| 13 | 813.2 | 52.4 | 1788 | 17 | AAV42805 | Murine Ikaro's gene |
| 14 | 813.2 | 52.4 | 1788 | 19 | AAV42805 | Murine Ikaro's cDNA |
| 15 | 813.2 | 52.4 | 1788 | 19 | AAV42805 | Murine Ikaro's cDNA |
| 16 | 811.6 | 52.3 | 1788 | 19 | AAV42805 | Murine Ikaro's cDNA |
| 17 | 689.4 | 44.4 | 1296 | 17 | AAV42805 | Murine Ikaro's iso |
| 18 | 689.4 | 44.4 | 1296 | 19 | AAV42805 | Murine Ikaro's cDNA |
| 19 | 689.4 | 44.4 | 1296 | 19 | AAV42805 | Murine Ikaro's cDNA |
| 20 | 680 | 43.8 | 714 | 19 | AAV42807 | Mouse Ikaro's iso |
| 21 | 577 | 37.2 | 1170 | 17 | AAV42807 | Mouse Ikaro's cDNA |
| 22 | 577 | 37.2 | 1170 | 19 | AAV42807 | Mouse Ikaro's cDNA |
| 23 | 573.8 | 37.0 | 1170 | 19 | AAV42809 | Mouse Ikaro's cDNA |
| 24 | 458.2 | 29.5 | 1128 | 17 | AAV42809 | Mouse Ikaro's cDNA |
| 25 | 458.2 | 29.5 | 1128 | 19 | AAV42809 | Mouse Ikaro's cDNA |
| 26 | 458.2 | 29.5 | 1128 | 19 | AAV42809 | Mouse Ikaro's cDNA |
| 27 | 457.2 | 29.5 | 708 | 19 | AAV42810 | Mouse Ikaro's cDNA |
| 28 | 411.8 | 26.6 | 1384 | 20 | AAV42810 | Mouse Ikaro's cDNA |
| 29 | 408.6 | 26.3 | 1384 | 20 | AAV42810 | Mouse Ikaro's cDNA |
| 30 | 404.2 | 26.1 | 1384 | 20 | AAV42810 | Mouse Ikaro's cDNA |
| 31 | 401.6 | 25.9 | 1327 | 20 | AAV42810 | Human Helios-2 cDN |
| 32 | 329.6 | 21.3 | 1520 | 20 | AAV42810 | Human Helios-2 cDN |
| 33 | 324 | 20.9 | 2688 | 21 | AAV42810 | Murine embryonic b |
| 34 | 255 | 16.4 | 255 | 19 | AAV42810 | Ikaro's protein enc |
| 35 | 234 | 15.1 | 270 | 19 | AAV42810 | Ikaro's protein enc |
| 36 | 223.2 | 14.4 | 270 | 19 | AAV42810 | Ikaro's protein enc |
| 37 | 216.4 | 14.0 | 628 | 18 | AAV42810 | Murine embryonic b |
| 38 | 216.4 | 14.0 | 628 | 18 | AAV42810 | Human Alolos parti |
| 39 | 168 | 10.8 | 168 | 19 | AAV42810 | Human Alolos cDNA |
| 40 | 145.8 | 9.4 | 514 | 22 | AAV42810 | Ikaro's protein enc |
| 41 | 145.8 | 9.4 | 523 | 22 | AAV42810 | Human cDNA encodin |
| 42 | 145.8 | 9.4 | 523 | 22 | AAV42810 | Human genomic DNA |
| 43 | 145.8 | 9.4 | 523 | 22 | AAV42810 | Human genomic DNA |
| 44 | 140.8 | 9.1 | 168 | 19 | AAV42810 | Human genomic DNA |
| 45 | 135 | 8.7 | 135 | 19 | AAV42810 | Ikaro's protein enc |

ALIGNMENTS

| | |
|----------|--|
| RESULT | 1 |
| AAV42840 | |
| ID | AAV42840 standard; cDNA; 1551 BP. |
| AC | AAV42840; |
| XX | 11-JAN-1999 (first entry) |
| DT | Human Ikaro's isoform h1k-1 cDNA. |
| DE | Ikaro's; h1k-1; transcription factor; human; lymphocyte; |
| KW | cell differentiation; T cell; cancer; immunodeficiency; |
| KW | Alzheimer's disease; therapy; diagnosis; ss. |
| XX | Homo sapiens. |
| OS | |
| XX | |
| PH | Key |
| FT | Location/Qualifiers |
| FT | 1..26 |
| FT | /*tag= a |
| FT | /number= Ex1 |
| FT | 27..163 |
| FT | /*tag= b |
| FT | /number= Ex2 |
| FT | 164..420 |
| FT | /*tag= c |
| FT | /number= Ex3 |
| FT | 421..588 |
| FT | /*tag= d |
| FT | /number= Ex4 |
| FT | 589..714 |
| FT | /*tag= e |
| FT | /number= Ex5 |

FT exon 715..849
FT /*tag= d
FT /number= Ex6
FT 850..1551
FT /*tag= e
FT /number= Ex7

CA2194256-A.

05-MAR-1998.

02-JAN-1997; 97CA-2194256.

05-SEP-1996; 96US-0711417.

(GEO) GEN HOSPITAL CORP.

Georgopoulos K;

WPI; 1998-378292/33.

P-PSDB; AAW70971.

New nucleic acid encoding Ikaros protein involved in early differentiation of lymphocytes - existing in several isoforms, and related products, used to treat e.g. immune diseases or cancer and to control cell differentiation

Claim 1; Page 127-129; 158pp; English.

This is the nucleotide of human Ikaros CDNA (isoform hik-1) that codes for a 516-amino acid zinc finger protein (see AAW70971) that is involved in the early differentiation of lymphocytes. It was isolated from a Jurkat T cell line library using mouse Ikaros exon 7 CDNA as probe. The Ikaros gene maps between p11.2-p13 on human chromosome 7. The human and murine Ikaros sequences (see AAW2805-11 and AAW2840) are highly conserved. Differential splicing of Ikaros gene transcripts gives rise to different Ikaros protein isoforms. The invention provides Ikaros nucleic acids, vectors and host cells expressing Ikaros proteins. These are used to treat T and B cell diseases (e.g. immune deficiencies caused by drugs, radiation or cancers), to control expression of heterologous genes placed under control of an Ikaros-responsive element, and to modulate cell division, amplification or differentiation, especially in haematopoietic cells. Some Ikaros isoforms are antagonistic of others and may be used to inhibit interaction with DNA sequences. The same effect can be achieved with Ikaros-binding oligonucleotides. Examining the expression of the Ikaros gene, or its allelic structure, can be used to assess risk of acquiring the above diseases.

Sequence 1551 BP; 393 A; 450 C; 443 G; 265 T; 0 other;

Query Match 100.08; Score 1551; DB 19; Length 1551;
Best Local Similarity 100.08; Pred. NO. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATCTGACGAGGGTCAAGACATGTCTTCTCATCAGGAGGAAAGCCCTGTA 60
DB 1 atggaTctgacagagggtcaagacatgtcttctcatcagggaagaaagccctgtga 60
QY 61 AGCGATATCCAGATGAGGGCGATGAGCCCATGCGGATCCCGAGGACCTCTCCACCA 120
DB 61 agcgatactcagatgagggcgatgagcccatgcccgaTccccggagacctctcaccacc 120
QY 121 TCGGAGGACAGCAAGCTCCAAAGAGTGACAGAGTCGTGGCCAGTAATGTTAAAGTAGAG 180
DB 121 tcggagagacagaaagctccaagatgacagatcgTggccagtaatgttaaagttagag 180
QY 181 ACTCAGAGTGATGAAGAGATGGCGTGCCTGTGAAATGAATGGGSAAGATGTCCGGAG 240
DB 181 actcagagtatgaagagaatggcgTgctgtgaaatgaatcggggaaagaatgttcggag 240

QY 241 GATTACGAATGCTTGTATGCTCGGGAGAGAAATGAATGGCTCCACAGGACCAAGGC 300
DB gattacgaatgcttgtatgctcgggagagaaatgaatggctccacagggaccaaggc 300
QY 301 AGCTCGGCTTTGTCGGGAGTTGGAGCATTCGACTTCTTAACGGAATAAGTGTGAT 360
DB agctcggctttgtcgggagttggaggcattcgacttcttaacggaataaagtgtgat 360
QY 361 ATCTGTGGATTCATTCGATCGGGCCCAATGTCTCATGTTTCAAAAAGACCACT 420
DB atctgtggatcatttgcacTcggggcccaatgtctcatggttcacaaaagaagccacact 420
QY 421 GGAGAACGGCCCTTCCAGTGCATTCAGTGGGGGCGCTTATTACCCAGAGGCGACCTG 480
DB ggagaacggcccttccagtgcaatcagtgcgggcctcattcccccagaagggcacctcg 480
QY 481 CTCGGGCACATCAAGCTGCATTCGGGGAGAGCCCTTCAATGCCACCTCTCAACTAC 540
DB ctccggcacatcaagctgcatTccggggaggaagcccttcaaatgccacotctgcaactac 540
QY 541 GCCTGCCCGGAGGAGCGCCCTCACTGGCCACCTGAGGAGCGACTCCGTTGGTAAACCT 600
DB gcctgcccgagggagagcgccctcactggccacctgaggacgcaactcgttggtaacct 600
QY 601 CACAAATGTGATATGTGGCGGAGAGCTATAACAGCGAACCTCTTTAGAGGACATAAAA 660
DB cacaatgtgatattgtggcggaagcTataaacagcgaaacgtcttttagaggaacataaa 660
QY 661 GAGCGCTGCCAACAATCTACTTTGAAAGCATGGGCGCTTCGGGCACACTGTACCCAGTATT 720
DB gagcgctgccacaactacttgaagagcatggccttccgggcacactgtaccctgattcatt 720
QY 721 AAAGAAGAATTAAGCACAGTGAATGGCAGAGACCTGTGCAAGATAGATCAGAGAGA 780
DB aaagaagaactaagcacagtgaatggcagaagacctgtgcaagatagatcagagaga 780
QY 781 TCCTCTGTCTGGACAGACTAGCAAGTAATGTGCGCAACAGTAAGAGTCTATGCCTCAG 840
DB tcctctgtctggacagactagcaagtaatgtcgccaaacgtaaagctctatgctctcag 840
QY 841 AAATTTCTGGGACAAAGGCGCTGTCGACACGCGCTTACGACAGTGCACAGTACGAGAG 900
DB aaatTTctgggacaaaggcctgctccgacagccctacacagtgccacgtacgagaag 900
QY 901 GAGAACAAATGATGAAGTCCACGCTGATGGACCAAGCATCAACACGCCATCAACTAC 960
DB gagaaacaaatgatgaagtcccacgtgatggaaccaagcctcaaacacccatcaactac 960
QY 961 CTGGGGCGGAGTCCCTGCGCCCGCTGGTGCAGACGCGCGCGGCGGCTTCCGAGGTGTC 1020
DB ctggggcgagtcctcgcccgctggtgtcagacgcccccgcggttccgaggtgggtc 1020
QY 1021 CCGGTATACGCGCGATGTACAGCTGCACAGGCGCTCGGAGGGCACCCGCGCTCAAC 1080
DB ccggtatcagcccgatgtaccagctgcacaggcgctcggagggcaccocgcgtccaac 1080
QY 1081 CACTCGGCGGACAGGACGCGCGCTGAGTACTGTCTGTCTCTCCAGGCGCAAGTGGTG 1140
DB cactcgccgagagcagcgcgctgagtcactcgtctgctctcctcaagggccaagtgggtg 1140
QY 1141 CCCTCGGAGCGGAGGCGCTCCCGAGCAACAGTGCACAGCTCCAGACCTCCAGGACCGAGAGC 1200
DB cctctcggagcgagcgctcccgagcaacagctgccaagactccagcgacacgagagc 1200
QY 1201 AACACAGAGGACGACGCGGCTTATCTACCTGACCAACACATCGCCGCGACGCGG 1260
DB aaacacgagagcagcgagcggtcttctcactgacaaacacacatcgccgacgcgcg 1260
QY 1261 CRACGCGTCTCGCTCAAGGAGGAGCAGCGCGCTACAGACTGTGTCGGCGCGCTCCGAG 1320
DB caacgcgctgctcgcTcaagagagcagcaccgcgctactacgacctgctgcgcgccctccgag 1320
QY 1321 AACTCGCAGACGCGCTCCCGTGGTGCAGCACCCAGCGGGAGCAGATGAAGGTGTACAAG 1380

Db 1321 aactcagcagcgcctccgctggtcagcaccagcgggagcagatgaagggttacaag 1380
 QY 1381 TCGGAACACTGCGGGGTGCTTCTCTGATCATCGTCTATGATACACATCCACATGGGCTGC 1440
 Db 1381 tgcgaacactgcgggtgctctctcctggtacacgtcatgtacacattccacatgggctgc 1440
 QY 1441 CACGGCTCCGATGATCCCTTTGAGTGCACATGTGCGGCTACACACAGGACCGGTAC 1500
 Db 1441 cagggctccgtgatcccttttgatgcaacatgtcggtacacacagcagccggtac 1500
 QY 1501 GAGTCTCTGCGCAGATCAACGCGAGGAGCAGCGCTTCCACATGAGCTAA 1551
 Db 1501 gaggttctcgtgcacataacgcgaggggagcaccgctccacatgagctaa 1551

RESULT 2

ID AAC76542 standard; cDNA; 6439 BP.

XX AAC76542;

DT 08-FEB-2001 (first entry)

DE Human ORFX ORF2097 polynucleotide sequence SEQ ID NO:4193.

XX Human; open reading frame; ORFX; detection; cytotatic; hepatotropic;
 KW vulnary; antipsoriatic; antiparkinsonian; nontropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiac;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive; ss.

OS Homo sapiens.

XX WO200058473-A2.

PN 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US08621.

XX 31-MAR-1999; 99US-0127607.

XX 02-APR-1999; 99US-0127636.

XX 05-APR-1999; 99US-0127728.

XX 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2000-602362/57.

XX P-PSDB; ABA42333.

PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -

PS Claim 5; Page 3386-3390; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytotatic; hepatotropic; vulnary;
 CC antipsoriatic; antiparkinsonian; nontropic; neuroprotective;
 CC osteopathic; anticonvulsant; antirheumatic; immunosuppressant;
 CC immunostimulant; cardiac; thrombolytic; coagulant; vasotropic;

CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy.
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC erythematosus, hypothyroidism, cholesterol ester storage, systemic lupus
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 6439 BP; 1721 A; 1568 C; 1498 G; 1652 T; 0 other;

Query Match 94.7%; Score 1468.8; DB 21; Length 6439;
 Best Local Similarity 97.7%; Pred. No. 0;
 Matches 1524; Conservative 0; Mismatches 27; Indels 9; Gaps 3;

QY 1 ATGGATGCTGACGAGGGTCAAGACATGTCTTCTCATCAGGGAAGAGCCCTCTGA 60
 Db 169 atggatgctgatgagggtcaagacatgtctcccaagtttcagggaagaaagccctgtg 228
 QY 61 AGCGATATCCAGATGAGGCGGATGAGCCATGCGGATGCCCGAGGACCTCTCCACACC 120
 Db 229 agcgatattccagatgaggcgatgagccatgagccatgagccatgagccatgagccatg 288
 QY 121 TCGGAGGACAGCAAGCTCCCAAGATGACAGAGTCGTGGCGCATGATGTTAAAGTAGAG 180
 Db 289 tcggaggacagcaagctcccaagatgacagagtcgtggccagtaattgtaagtagag 348
 QY 181 ACTCAGATGATGAGAGATGAGGCGTGCCTCTGAAATGAATGGGGAAGATGTGGCGAG 240
 Db 349 actcagatgataagagaatggcgctgctgtaaatgaatgaatgggaagatgtggagag 408
 QY 241 GATTTACGAATGCTTGTGCTCGGAGAGAAATGAATGCTCCACAGGAGCAAGGC 300
 Db 409 gatttacaagatgctgtgctcctcgaggagaaatgaatgctccacagggaccagagc 468
 QY 301 AGCTCGGCTTGTGCGGAGTTGGAGGCAATTCGACTTCTTAACGGAAACTAAAGTGTGAT 360
 Db 469 agctcggcttgtcggagttggagggcatttccttaacgaaactaaagttgtgat 528
 QY 361 ATCTGTGGGATCATTGTCATCGGCGCCCAATGTGCTATGTTTCAAAAAGAGCCACACT 420
 Db 529 atctgtgggatacttgcctcggcccaatgtgctcatggttcacaaaagaagccact 588
 QY 421 GGAGAAGGCCCTTCCAGTGCATTCAGTGGGGGCGCTCATTACCCAGAGGCAACCTTG 480
 Db 589 ggagaacggcccttccagtgcaatcagtgcgggcctcattcaccacagaagggcaacctg 648
 QY 481 CTCGCGCACATCAAGCTGCATTCGCGGGAAGAGCCCTTCAATGCCACACTCTGCAACTAC 540
 Db 649 ctcggcacatcaagctgcatctccgggagagcccttcaaatgccacctctgcaactac 708
 QY 541 GCCTGCCCGCGGAGGAGCGCCCTCACTGGCGGCGCTCATTACCCAGAGGCAACCTTG 600
 Db 709 gcctgccgcgagggagcgcctcactggccacctggagcagcactccgttggtaacct 768
 QY 601 CACAATGTGGATATTGTGGCGGAAGCTATAACAGCGCAACCTCTTTAGAGGAACATAAA 660
 Db 769 cacaatgtggattgtggcgaagctataaacacagcagagctcttttagaggaacataaa 828
 QY 661 GAGCGTGCACAACTACTTGGAAAGCATGGCCCTTCGGGCGACACTGTACCCAGTCAAT 720
 Db 829 gacgctgcacaactacttggaaagcatggcccttcgggacactgtacccagtcatt 888
 QY 721 AAGAAGAACTAAGCACAGTGAATGGCAGAAAGACCTGTGCAAGATAGATCAGAGAGA 780
 Db 721 aagaagaaactaagcacagtgaatggcagaaagacctgtgcaagatagatcagagaga

RESULT 3
AAT16060
20010600 standard. CDNA: 1386 BP.

RESULT 3
AAT16060 standard: CDNA: 1386 BP.

| | | | | |
|-----------------------|---------|--------------------|-----------|--------------|
| Query Match | 89.4%; | Score 1386; | DB 17; | Length 1386; |
| Best Local Similarity | 100.0%; | Pred. NO. 3.e-301; | | |
| Conservative | 0; | Mismatches 0; | Indels 0; | Gaps |

| Query Match | 89.4% | Score 1386; | DB 17; | Length 1386; |
|-----------------------|---|---------------------|-----------|--------------|
| Best Local Similarity | 100.0%; | Pred. No. 3.3e-301; | | |
| Matches 1386; | Conservative | 0; Mismatches | 0; Indels | 0; Gaps |
| 166 | ANTGTTTAAAGTACAGAGACTCAGAGTGTATGAAGAGAATGGCGCTGCCTGTGTGAATGAATGAATGGG | 225 | | |
| | | | | |
| 1 | aatgttaaaatgagagactcagagatgatgaagagaatggcgctgtggaatgaatgaatggg | 60 | | |
| | | | | |
| 226 | GAAGAATGTGCGGAGGATTTACAAATGCTTGATGCTCGGGAGAGAAAAATGAATGGGTCC | 285 | | |
| | | | | |
| 61 | gaagaatgtgcgagagattcacgaatgcttgatgcttcggagagagaaatgaatggctcc | 120 | | |
| | | | | |
| 286 | CACAGGACCAAGGCAGCTCGGCTTTGTGCGGAGTTGGAGGCATTCGACTTCCTAACGGA | 345 | | |
| | | | | |
| 121 | cacagggaaccaagcagctcggtttgtcgggagtttggagggcatcgcactctctaacgga | 180 | | |
| | | | | |
| 346 | AAACTTAAAGTGTGATATCTCTGGGATCATTTGGCATCGGGCCCAATGTGCTCATGTTTCAAC | 405 | | |
| | | | | |
| 181 | aaactaaagtgtgatatctgtggatcatttgtcatcgggcccaatgtgtcatgtgtttcac | 240 | | |
| | | | | |
| 406 | AAAGAAGCCACACTGGAGACGGCCCTTCAGTGAATTCAGTGCGGGGCCCTCATTCACC | 465 | | |

[illegible]

CC disorder. It may also be used for assessing whether a subject is at
 CC risk for an immune disorder. It is of particular use in treating a
 CC disorder of the corpus striatum.

XX Sequence 1611 BP; 375 A; 484 C; 480 G; 272 T; 0 other;

Query Match 89.18; Score 1382.4; DB 15; Length 1611;
 Best Local Similarity 99.6%; Pred. No. 2.2e-300;
 Matches 1386; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 160 GCCAGTAATGTTAAAGTAGAGACTCAGAGTATCAAGAGAAATGGGCTGTGAAATG 219
 Db 217 gccagtaagttaaagttagagactcagagtcgatgaagagaatgggctgtgaaatg 276

QY 220 AATGGGAGAAATGTCGGAGGATTTACGAATGCTTTCATGCCCTCGGAGAGAAATGAT 279
 Db 277 aatgggaagaatgtgcggagatttacgaatctgatgcctcggagagaagaatgat 336

QY 280 GGCTCCACAGGACCAAGGACAGCTGGCTTTCGGGAGTGGAGCAATTCGACTTCT 339
 Db 337 ggcctccacagggacaaagcagctggcttgcggagttggaggttcgacttct 396

QY 340 AACGGAAACTAAAGTGTGATATCTGTGGATCATTTGATCGGAGTGGAGCAATTCGACTTCT 399
 Db 397 aacggaaactaaagtgtgatctgtggtatcatttgcattcggcccaatgtgctcatg 456

QY 400 GTTCACAAAAGAGCCACACTCGAGAACCGCCCTTCAGTGCATTCAGTGGGGCCCTCA 459
 Db 457 gtccacaaaagagccacactcgagaaagcccttcacagtgcattcagtcgaggccctca 516

QY 460 TTACCCAGAGGCAACCTGCTCGGCACATCAAGCTCAAGTGCATTCGGGGAGAAAGCCCTTC 519
 Db 517 ttaccacagaaggcaacctgtcccgcaacatcaagctgcattcggggagaagcccttc 576

QY 520 AAATGCCACTCTGCAACTTACGCTTCCGCGGAGGAGCGCCCTACTGGCCACTGAGG 579
 Db 577 aaatgccactctgcaacttacgcttccgcccggaggagcgccctcactggccactgag 636

QY 580 AGCAGCTCGTGTGTAACCTCACAAATGTGGATATTGTGGCCGAAGCTATAACAGCGA 639
 Db 637 agcagctcgtgtgtaaacctcacaatgtggaatattgtgcccgaagctataacagcga 696

QY 640 ACGCTTTTAGAGGAACATAAAGAGCGTGCACAACTACTTTGAAAGCATGGCCCTTCCG 699
 Db 697 acgcttttagaggaaacataaagagcgtgcacaactacttggaaagcatgggcccctcg 756

QY 700 GCCACACTGTACCCAGTCAATTAAGAGAACTAAGCACAGTCAATGGCAGAGACCTG 759
 Db 757 ggcacactgtaccagtcatttaagaagaactaaagcacagtgaaatggcagaagacctg 816

QY 760 TGCAAGATAGGATCAGAGAGATCTCTGCTGGACAGACTAGCAAGTAAATGCGCAAA 819
 Db 817 tgcaagataggatcagagagatctctgctggacagactagcaagttaatgtcgccaaa 876

QY 820 CGTAAGAGCTCTATGCTCAGAAATTTCTTGGGCAAGGCGCTGCCACAGCCCTAC 879
 Db 877 cgtgaagactctatgctcagaaatttcttgggacaagggcgtcccgacacgcccctac 936

QY 880 GACAGTCCACAGTACGAGAGGAGACGAAATGATGAAGTCCCATGATGGACCAAGCC 939
 Db 937 gacagtccaagtacgagaaggagaaatgatgaagtcaccatgtagggaccaagcc 996

QY 940 ATCAACAGCCATCAACTACTTGGGGCCGAGTCCCTGCGCCGCTGTCAGACGCCC 999
 Db 997 atcaacagccatcaactacttggggccgagtccttgcgcccgtgtgtcagacgcc 1056

QY 1000 CCGGGCGGTTCCGAGTGTCCCGGTATCATGCCCGCATGTTACCAAGTGCAGAGCGCTCG 1059
 Db 1057 ccgggcggttccgagtggtcccggtatcatcagccgatgtaccagctgcacagcgctcg 1116

QY 1060 GAGGCAACCCCGCTTCCACCACTCGCGCCAGGACAGCGCGCTGGAGTACCTGCTGCTG 1119
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1117 gagggcaccocgcgtccaccactcggccaggaagcgcgtgagtagctgctgctg 1176
 QY 1120 CTCTCAAGGCCAAGTGGTGCCTCGAGCGCGAGCGCTCCCGAGCAACAGCTGCCAA 1179
 Db 1177 ctctcaagggccaaagtgtgctcctcgagcgagcgagggcgctcccccagacagctgcca 1236
 QY 1180 GACTCCAGGACACCGAGAGCAACAGAGGAGCAGCGGCTTTATCTACCTGACC 1239
 Db 1237 gactccacgacacccagagcaacaagcagcgagcgagcggttcttctacctgacc 1296
 QY 1240 AACCACTCGCCCGACCGCGGCGCAACGCGTCTCAAGGAGGAGCAGCGCGCTACGAC 1299
 Db 1297 aaccacatcccccagcgcgcgaacgcgtgtcgtcaagagagacacgcgcctacgac 1356
 QY 1300 CTGTCGCGCGCGCTCCGAGAACTCGCAGGAGCGCGCTCGGCTGCTCAGCAGCGGG 1359
 Db 1357 ctgctgcgcgcgcctccggaactcgcgagcggttccgcgtggtcagcaccagcg 1416
 QY 1360 GAGCAGATGAAGTGTACAGTGCAGAACACTGCGGGGTCTCTCTGGATCAGCTCATG 1419
 Db 1417 gagcagatgaaggtgtacaagtgcgaacactgcgggtgctcttctggtacacgctcatg 1476
 QY 1420 TACACATCCACATGGGCTGCCACGCTTCCGCTGATCCTTTTGTAGTCAACATGTGCGGC 1479
 Db 1477 tacaccatccaatgggctgcgcagcggttcggtatccttctgagtgaccatgtgcggc 1536
 QY 1480 TACCAGCCAGGACCGGTACGAGTTCTCGTGCACATAACGCGAGGGAGCAGCGCTTC 1539
 Db 1537 taccacagccagcggttaccaggttctcgtcgacataacgcgaggggagcaccgcttc 1596

QY 1540 CACATGAGCTAA 1551
 ||||||| |||

Db 1597 cacatgaagtaa 1608

RESULT 6
 AAV42806
 ID AAV42806 standard; cDNA; 1386 BP.
 XX
 AC AAV42806;
 XX
 DT 11-JAN-1999 (first entry)
 XX Human Ikaros isoform hrk-1 cDNA.
 XX
 DE Ikaros; hrk-1; transcription factor; human; lymphocyte;
 cell differentiation; T cell; cancer; immunodeficiency;
 Alzheimer's disease; therapy; diagnosis; ss.
 KW
 KW
 KW
 XX
 OS Homo sapiens.
 XX
 FH Key
 exon Location/Qualifiers
 1..255
 /tag= a
 /number= Ex3
 256..423
 /tag= b
 /number= Ex4
 424..549
 /tag= c
 /number= Ex5
 550..684
 /tag= d
 /number= Ex6
 685..1386
 /tag= e
 /number= Ex7

CA2194256-A.
 05-MAR-1998.
 02-JAN-1997; 97CA-2194256.

Db 703 ctgcggcacatcaagtgcactcgggtgagaagcccttcaaatgccatctttgcaactat 762
QY 541 GCCTGCCCGCGGAGGAGCGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAAACCT 600
Db 763 gctgcgcgcggagggagcgcctcaaccgcccacctgagcagcactcgttggtaagcct 822
QY 601 CACAAATGTGGATATTGGCGGAGCTATAAACAGGCAAGCGTCTTTAGAGGAAACATAA 660
Db 823 cacaatgtgatatgtggcggagcgtataaacagcgaagcctctttagaggagcataaa 882
QY 661 GAGCCGCTGCCAACAATACTTGAAGCATGGGCTTCGGGCGACACTGTACCCAGTCATT 720
Db 883 gagcagatgccacaactcttgaagcatggccttcgggc---gtgtgccagtcatt 939
QY 721 AAAGAAGAACTAAGCAGACGTAATGGCAGAGACCTGTGCAAGATAGATCAGAGAGA 780
Db 940 aaggaagaataaccacacagatgagcagagacgtgtgcaagacgtgtgcaagatagagcagaggg 999
QY 781 TCTCTGTGTGGAGACTAGCAAGTAATGTGCCAAACGTAAGAGCTTATGCTCTCAG 840
Db 1000 tccctgtcctggacaggctggcaagcaatgtgcgaacagtaagagcctctatgcctcag 1059
QY 841 AAATTTCTTGGGACAGGCGCTGTCCGACACGCCCTAGCAGATGCCACGTCACGAGAG 900
Db 1060 aaattcttgagacaagtgcctgtcagacatgcctctatgacagtgcacactatgagaag 1119
QY 901 GAGAACAAATGATGAATCCACGTCATGGACCAAGCCATCAACACACCCATCACTAC 960
Db 1120 gag---gatgatgacatccacagctgatggaccagggccatcaaatgccaactac 1176
QY 961 CTGGGGCGGAGTCCCTGCGCCGCTGTGTCAGACGCCGCCGGGGTTCAGAGTGGTC 1020
Db 1177 ctggggctgtgctccctggcccttggtgcagacaccccccgttagctcgaggtgtg 1236
QY 1021 CCGGTATCATAGCCCGATGTACAGCTGCACAGS---CGTCCGAGGGACACCCCGCTCC 1077
Db 1237 ccagtcatcagctccatgtaccagctgcagacgccccctcagatggccccccacggctc 1296
QY 1078 AACCACTCGCCAGGACAGCGCGTGGAGTACCTGCTGCTCTCCAAAGCCCAAGTTG 1137
Db 1297 aaccattcagcacaga---cgccgtggataactgtcgtgctcacaagcccaagtct 1353
QY 1138 GTGCGCTCGGAGCGCGGAGCGTCCCGACACACAGCTGCCAAGACTCCACGACACCCGAG 1197
Db 1354 gtgtcatcggagcagagagcgcctcccccagcagacagctgccaagactccacagatacagag 1413
QY 1198 AGCAACACAGGAGCAGCGCAGCGGTCTTATCTACCTGACCAACCAACATCGCCCGACGC 1257
Db 1414 agcaacgaggaagaaacagcagcggccttatctacctaaccacacacatacccccagcat 1473
QY 1258 GCGC---AACGCGTGTCTCAAGAGGAGACACCGCGCTTACGACCTGCTCGCGCGCGCC 1314
Db 1474 gcagcaatggcgtggtcctcctcaagagagcagcgcctacagaggtgctgagggcgcc 1533
QY 1315 TCCGAGAACTCGCAGAGCGCGTCCGCTGTGTCAGCACCAGCGGGAGCAGATGAAGGTG 1374
Db 1534 tcagagaactcgcagatgctcctcggtgtggaacagcaggtggtgagcaggtgaggtg 1593
QY 1375 TACAACTCGGACACTGCCGGGTGCTTCTCTGATCAGCTATGATACACATCCACATG 1434
Db 1594 tacaagtgcacactgcccgtgctcctcctggtgacgctcagctatgataccattcagctg 1653
QY 1435 -----GGCTGCGCAGCGCTCCGTTGATCTTTTGTAGTGCACATGTGCGGCTACCA 1485
Db 1654 ggcgtgcagtgctgcattgcttccggtggtatcccttggatgtatcagctgtgtgtatc 1713
QY 1486 ACCGAGACCGGTACGAGTTCTGTCGACATAAACCGGAGGAGCAGCCGCTTCCACATG 1545
Db 1714 agccagacaggtacgagttctcatccatccatcacgcggtggagcagctgttaccacctg 1773
QY 1546 AGCTAA 1551
Db 1774 agctaa 1779

RESULT 9

AAV42808

ID AAV42808 standard; cDNA; 2049 BP.

XX AC AAV42808;

XX DT 11-JAN-1999 (first entry)

XX DE Mouse Ikaros isoform mk-1 cDNA.

XX KW Ikaros; mk-1; transcription factor; mouse; lymphocyte;
cell differentiation; T cell; cancer; immunodeficiency;
Alzheimer's disease; therapy; diagnosis; ss.

XX OS Mus sp.

XX FH Key Location/Qualifiers

FT CDS 223..1779

FT exon /tag= a

FT exon 223..384

FT exon /tag= b

FT exon /number= Ex1/2

FT exon /tag= c

FT exon /number= Ex3

FT exon /tag= d

FT exon /number= Ex4

FT exon /tag= e

FT exon /number= Ex5

FT exon /tag= f

FT exon /number= Ex6

FT exon /tag= g

FT exon /number= Ex7

XX CA2194256-A.

XX PD 05-MAR-1998.

XX PF 02-JAN-1997; 97CA-2194256.

XX PR 05-SEP-1996; 96US-0711417.

XX PA (GEO) GEN HOSPITAL CORP.

XX PI Georgopoulos K;

XX DR WPI; 1998-378292/33.

XX P-PSDB; AAW70966.

XX PT New nucleic acid encoding Ikaros protein involved in early

XX PT differentiation of lymphocytes - existing in several isoforms, and

XX PT related products, used to treat e.g. immune diseases or cancer and

XX PT to control cell differentiation

XX PS Claim 7; Page 75-77; 158pp; English.

XX CC This is the nucleotide of mouse Ikaros cDNA (isoform mk-1) that

XX CC codes for a 518-amino acid zinc finger protein (see AAW70966) that

XX CC involved in the early differentiation of lymphocytes. mk-1 cDNA

XX CC was isolated from a mature murine T cell line E14 library using a

XX CC 300 bp fragment from the 3' end of mk-2 cDNA (see AAV42805) as

XX CC probe. 5 Different isoforms of mouse Ikaros (see AAV42805) and

XX CC AAV42807-10) have been identified. These arise by differential

XX CC splicing of Ikaros gene transcripts. Isoform mk-1 contains all 7

XX CC exons. It is abundantly expressed in the early foetal liver, the

XX CC maturing thymus and the postnatal spleen. The Ikaros gene is

XX CC located at the proximal arm of murine chromosome 11. Ikaros

sequence 2049 BP; 514 A; 531 C; 574 G; 430 T; 0 other;

| | | | |
|----|-----|---|-----|
| QY | 1 | ATGGATGCTTGCAGAGGGTCAAGACATGTCCTTCATCAGGAAGAAAGCCGCCCTGTA | 60 |
| Db | 223 | atggaagtgcga tgaagggtcaagaacatgtcccaagtttcagaaggagagccccccagtc | 282 |
| QY | 61 | AGCGATACTCCAGATGAGGGCGATGAGCCATGCCGATGCCCGAGGACCTCTCCACACCC | 120 |
| Db | 283 | agtgcacatccagatgaagggtgagccatgtcctgtgagcagcctgtcccaactacc | 342 |
| QY | 121 | TCCGGAGGACAGCAAGCTCCAAGAGTACACAGAGTCGTGGCCAGTAATGTTTAAAGTAGAG | 180 |
| Db | 343 | tcctggagcacagcagaactccaaagatgatcgagcatggtccagtaattgtlaaagtagag | 402 |
| QY | 181 | ACTCAGAGTGATGAAGAGAAATGGCGTGCTGTGAAATGAATGGGAGGAAGATGTGCGGAG | 240 |
| Db | 403 | actcagaagtatgaagagaatgggtgctgtgaaatgaa tggggaaagaaatgtgcagag | 462 |
| QY | 241 | GATTACGAATGCTTGATGCTCGGAGAGAAAAATGAATGGCTCCACAGGACCAAGGC | 300 |
| Db | 463 | gatttacaagatgcttgatgctcctcgagagagaaaaatgaa tggctccacagggacccaagtc | 522 |
| QY | 301 | AGCTCGCGCTTTGCGGAGTTGAGGCATTCGACTCTCTTAACGGAAAACTAAGTGTCAT | 360 |
| Db | 523 | agctcgctttgtcaggagttgaggcatctgcactcctaa cggaaaaactaaatgaatgtat | 582 |
| QY | 361 | ATCTGTGGATCATTTGCATCGGGCCCAATGTCTCATGTGTTACAAAAAGAGCCACACT | 420 |
| Db | 583 | atctgtgggaatcg tttgcac tggggcccaatgtgctcatggttcacaaaagaagtcatact | 642 |
| QY | 421 | GGAAAGAGGCCCTTCCAGTGCATCAGTGGGGGCGCTCATTCACCAGAAAGGCGACCTG | 480 |
| Db | 643 | ggtgaagcgcccttccagtgcaaccagatctggggcctctttaccagaaagagcaacctc | 702 |
| QY | 481 | CTCGGCACATCAGCTGCATTCGGGGAGAGCGCTTCAAATGCCACCTCTGCAACTAC | 540 |
| Db | 703 | cttgggcacatcaagctgcactctgg tgaagaccccttcaaatgcocatctttgcaactat | 762 |
| QY | 541 | GCCTCGCGCGGAGGAGCGCCTCACTGGCCACCTGAGGACGCACTCCCGTTGTTAAACCT | 600 |
| Db | 763 | gcctcgcccgaggaggcgccctcacgcgcacctgaggcgcactcgtgtgtgaagcct | 822 |
| QY | 601 | CACAATGTGATATTGTGGCCGAGCTATAACACAGCGAACGTCCTTTAGAGGAACATAAA | 660 |
| Db | 823 | cacaatgtgatattgtggccgagctataaacagcgaagcctcttttagagagagcataaa | 882 |
| QY | 661 | GAGCGCTGCACAACCTACTTGGAAAGCATGGCCCTTCGGGCACACTGTATCCACGATCAT | 720 |
| Db | 883 | gagcgatgccacaactacttgaaaagcatgggcttcgggccc---g tgtgccagtcatt | 939 |
| QY | 721 | AAAGAGAAACTTAACGACAGTGAATGCGACAAGACCTGTGCAAGATAGGATCAGAGAGA | 780 |

RESULT 10

AC AAT16065;

09-MAY-1996 (first entry)

Tkaros cDNA.

xx Ikaros; transgene; transgenic animal; transgenic mouse;
kw immunocomprised; immune system disorder; nervous system disorder;
kw animal model; ss.
kw

OS Not specified.
 PN WO9604372-A1.
 XX 15-FEB-1996.
 PD
 XX 28-JUL-1995; 95WO-US09345.
 XX
 XX 29-JUL-1994; 94US-0283300.
 XX
 XX (GEHO) GEN HOSPITAL CORP.
 XX
 XX Georgopoulos K;
 PI
 XX WPI; 1996-129389/13.
 DR P-PSDB; AAR92020.
 XX
 PT Transgenic rodent having Ikaros trans-gene (pref. mutated) - is
 PT severely immuno-compromised and can be used as model to determine
 PT effects of treatment for immune and nervous system disorders
 XX
 PS Disclosure; Page 71-73; 102pp; English.
 XX
 CC A CDNA clone (AAT16065) coding for an Ikaros protein (AAR92020) has
 CC been identified. Transgenic animals, pref. mice, having a
 CC mutated Ikaros transgene, esp. a mutation that alters the DNA
 CC binding domain of the Ikaros protein, are used as models to
 CC determine the effects of treatments for immune or nervous system
 CC disorders.
 XX
 SQ Sequence 1004 BP; 235 A; 328 C; 286 G; 155 T; 0 other;

Query Match 56.0%; Score 868; DB 17; Length 1004;
 Best Local Similarity 88.8%; Pred. No. 3.8e-185;
 Matches 1004; Conservative 0; Mismatches 0; Indels 126; Gaps 1;

QY 421 GGAGAGCGCCCTCCAGTCAATCAGTGGGGGCTTATTCACCCAGAGGCGCAACCTG 480
 DB 1 ggaagacggccctccagtgcaatcagtgcgggccctattccaccagaagggaacctg 60
 QY 481 CTCGGGCACATCAAGCTGCATTCGGGGAGAGCCCTTCAATGGCCACTCTGCAACTAC 540
 DB 61 ctccggcacatcagctgcattccggggagagccctcaaatgcaacctctgcaactac 120
 QY 541 GCTGCGCGCGGAGGAGCGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAACTT 600
 DB 121 gcttgcgcgcggaggagcgcctcactgcccactgagagcgcactcc----- 168
 QY 601 CACAAATGTGGATATTGTGGCCGAAGCTATAACAGCGGAACGCTTTTAGAGGAACATAAA 660
 DB 169 ----- 168
 QY 661 GAGCGTGGCCACAACTACTTGGAAAGCATGGGCCCTTCGGGGCACACTGTACCCAGTCA 720
 DB 169 -----gtcatt 174
 QY 721 AAGAGAAGAACTAAGCACAGTGAATGGCAGAGACCTGTGCAAGATAGGATCAGAGAGA 780
 DB 175 aaagaagaactaagcacagtgaatggcagaagacctgtgcaagatagatcagagaga 234
 QY 781 TCTCTCGTCTGACAGACTAGCAAGTAATGTCGCCAAGCACTAAGAGCTCTATGCCCTCAG 840
 DB 235 tctctcgtctggaagactagcaagtaattgtcccaaacgtaagagctctatgcctcag 294
 QY 841 AAATTTCTTGGGCAAGGGCTGTTCGCACACAGCGCCCTACGACAGTGCACGCTACGAGAA 900
 DB 295 aaatttcttgggacaaggcctgtccgacacgcccctacgacagtcgcaactcagaga 354
 QY 901 GAGAGGAATGATCAAGTCCCAAGTGTATGACCAAGCCATCAACAGCGCATCAACTAC 960
 DB 355 gagaacgaatgatgaagtcccaagctgatggaccaagccatcaacaacgcatcaactac 414

QY 961 CTGGGGCGCGAGTCCCTCGCGCCCGCTGTGCAGAGCCCGCGGGGCTTCGAGGTGGTC 1020
 DB 415 ctgggggcccagtgctccctcgcccgtgtgtagacgccccggcggttccgaggtggtc 474
 QY 1021 CCGGTATCAGCCCGATGTACAGCTGCACAGGGGCTCGGAGGCGACCCCGCGCTCCAAC 1080
 DB 475 ccggtatcagcccgatgtaccagtgacagcgctcgaggggaccccgctcccaac 534
 QY 1081 CACTCGGCCAGGACAGCGCGGTGAGTACCTGTGTCTCCAAAGGCCAAAGTTGGTG 1140
 DB 535 cactcggccagggacagcgccgtgagttacctgtgtctctccaagggcgaagtgggtg 594
 QY 1141 CCTCGAGCGCGAGCGCTCCCGAGCAACAGCTGCCAAGACTCCACGGGACCGGAGAGC 1200
 DB 595 cctcggagcgagggcgctcccgagcaacagctgccaagactccacggagacagagc 654
 QY 1201 AACACAGAGGAGCGAGCGCGGTCTTATCTACCTGACCAACACACATCGCCGACGCGG 1260
 DB 655 aacaacgaggagcagcgcggtcttatctacctgaccaaccacatcgccgagcgcg 714
 QY 1261 CAACGCGTGTGCTCAAGGAGGAGCACCGCGCTTACGACCTGTGCGCGCGCTCCGAG 1320
 DB 715 caacgctgtctctcaaggaggagcaccgctgctacgacctgtgctgcgctccgag 774
 QY 1321 AACTCGCAGGACGCGCTCCCGGTGTGTCAGCACCGGCGGAGCAGATGAAGTGTACAAG 1380
 DB 775 aactcgcagagcgcgctcccggtgtgtcagcaccagcggggagcagatgaagtgtaag 834
 QY 1381 TGCGAACACTGCGCGGTGCTCTCTCTGGATCAGCTCATGTACACCATCCACATGGGCTGC 1440
 DB 835 tgcgaacactgcccgggtgctctctcttgatcaogtcatgtacaccatccacatggctgc 894
 QY 1441 CACGCTTCCGTGATCTTTTGTAGTGCACATGTGCGGCTTACACAGCGGACCGGTAC 1500
 DB 895 cagcgttcgctgctctctttgagtgcaacatgtgctgctacacagcagaccgggtac 954
 QY 1501 GAGTCTCTCGCACATAAGCGGAGGAGCACCGGCTTCCACATGAGCTA 1550
 DB 955 gagtctctgcacataacgcgaggggagcaccgcttccacatgagcta 1004

RESULT 11
 AAV66974
 ID AAV66974 standard; cDNA; 1004 BP.
 XX AAV66974;
 AC AAV66974;
 XX
 DT 14-JAN-1999 (first entry)
 XX
 DE Ikaros isoform encoding cDNA.
 XX
 KW CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;
 KW differentiation marker; immune system; corpus striatum; AIDS;
 KW Alzheimer's disease; ss.
 XX
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 CDS 1..1004
 FT /*tag= a
 FT /product= "Ikaros isoform"
 FT /note= "no stop codon given"
 XX
 PN US5824770-A.
 XX
 PD 20-OCT-1998.
 XX
 XX 05-JUN-1995; 95US-0465590.
 XX
 PR 02-MAY-1994; 94US-0238212.
 PR 14-SEP-1992; 92US-0946233.
 PR 14-SEP-1993; 93US-0121438.
 PR 05-JUN-1995; 95US-0465590.

XX PS Disclosure; Column 51-56; 111pp; English.

The present invention describes a purified peptide having at least one of the following properties: (a) it stimulates transcription of a DNA sequence under the control of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of Ikaros binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (d) it naturally occurring Ikaros isoform to any of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (e) it competitively inhibits the binding of a delta A element, an NFkB element or an Ikaros binding oligonucleotide consensus sequence; (f) it competitively inhibits Ikaros binding to Ikaros responsive elements; or (g) it inhibits protein-protein interactions of transcriptional complexes formed with naturally occurring Ikaros isoforms. The proteins, provided that they stimulate gene transcription under the control of delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides, delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides, competitively inhibit binding of naturally occurring Ikaros isoforms to delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides, competitively inhibit Ikaros binding to Ikaros-responsive elements and/or inhibit protein-protein interactions of transcriptional complexes with naturally occurring Ikaros isoforms, can be used to treat immune system disorders, e.g. leukemia or AIDS, or corpus striatum disorders, e.g. Alzheimer's disease. The present sequence encodes a specifically claimed mouse Ikaros protein.

XX SQ Sequence 1788 BP; 437 A; 486 C; 495 G; 370 T; 0 other;

Query Match 52.4%; Score 813.2; DB 19; Length 1788;
Best Local Similarity 85.5%; Pred. NO. 8.3e-173;
Matches 983; Conservative 0; Mismatches 143; Indels 24; Gaps 6;

| | | | |
|----|-----|--|------|
| QY | 417 | CACCTGGAGAACGGCCCTCCAGTSCAATCAGTCGCGGGGCTCATTCACCCAGAGGGCAA | 476 |
| Db | 378 | catgggtgaacggcctttccagtgcaaccagtcgtggcctctttaccacagaaggcaa | 437 |
| QY | 477 | CCTGCTCGGGCAGATCAAGCTGATTCGCGGGAGAGCCCTTCAATGCGACCTCTGCAA | 536 |
| Db | 438 | cctcctgaggcacatcaagctgcactcgtgggagagagcccttcaaatgcatctttgcaa | 497 |
| QY | 537 | CTAGCGCTGCCGGGAGGAGCGCCCTCACTGCGCCACCTGAGACGACCTCGGTGGTAA | 596 |
| Db | 498 | ctatgctgcgcggagggagcgcctccacggcgccactgaggacgcaactccgttggttaa | 557 |
| QY | 597 | ACCTCACAAATGTGGATATTGTGCCCGAAGCTATAACACGGAACGCTCTTTAGAGGAACA | 656 |
| Db | 558 | gctcacaaatgtggatatgtggccggagcctaataacagcgaagctcttttagaggagca | 617 |
| QY | 657 | TAAAGAGCGCTGCCAACACTACTTTGGAAGCANTGGCGCTTCCGGGGCACACTGTACCCAGT | 716 |
| Db | 618 | taagagcgatgccaactacttggaagcatggccttccgggc---gtgtgcccagt | 674 |
| QY | 717 | CATTAAAGAGAACTAGACAGTGAATGGCAGAGAGCTGTGCAAGATAGGATCAGA | 776 |
| Db | 675 | cattaaggaagaactaacaccacagagatggtgagagagacctgtgcaagataggagcaga | 734 |
| QY | 777 | GAGATCTCTGCTGCGGACAGCTAGCAAGTAATGTGCCAAACGTAAGAGCTCTATGCC | 836 |
| Db | 735 | gaagtccttgcctggagcaggtgtggcaagcaatgtcgcaaacgtgaagagctctatgcc | 794 |
| QY | 837 | TCAGAAATTTCTGGGGACAGGGCGCTCCGACACGCGCTACGACAGTGCACGTACGA | 896 |
| Db | 795 | tcagaaattcttgagacaagtgccgtgtcagacatgccctatgacagtgccaaactatga | 854 |
| QY | 897 | GAAGGAGACGAAATGATGAAGTCCACGTGATGACCAAGCCATCAACACGCCATCAA | 956 |
| Db | 855 | gaaggag---gatagatgacatccacagtgatggaccaggccatcaacaatgccaatcaa | 911 |
| QY | 957 | CTACCTGGGGCGGAGTCCCTGGCCCGCTGCTGCGAGACGCGCGCGGCTCCGAGGT | 1016 |
| Db | 912 | ctacctgggggctgagtcctgcccatttggtgcagacacaccccccccggtagctccaggt | 971 |

Search completed: August 28, 2002, 09:07:31
Job time: 4271 sec

| | | | |
|----|------|---|------|
| QY | 1017 | GGTCCCGGTTCATCAGCCCGGATGTACCAAGTGCACAGCGG---CTCGAGGGGACCCCGCG | 1073 |
| Db | 972 | ggtgccagtcagctccatgtaccagctgcacaagccccctcagatggccccccagc | 1031 |
| QY | 1074 | CTCAACCACTTCGGCCCGACAGACGCGGTGGAGTACCTGCTCTCTCAAGGCCAA | 1133 |
| Db | 1032 | gtccaaaccattcagcacagga---cgccgtggataactgtctgtctccaaagccaa | 1088 |
| QY | 1134 | GTTGGTCCCTCGAGCGCGGAGGCGGTCCCGAGCAACAGCTGCAAGACTCCACGACAC | 1193 |
| Db | 1089 | gtctgtgtcatcggagcgagagcctcccccagcaaacagctgccaagactccacagatac | 1148 |
| QY | 1194 | CGAGAGCAACCAACAGGAGGAGCGACGCGGTCTTACTTACCTACCAACCACTCCGCC | 1253 |
| Db | 1149 | agagagcaacggaggaggaacagcgagcgcccttatctactaaccaacacacacccc | 1208 |
| QY | 1254 | ACGCGCGG---AACCGCTGTGCTCAAGGAGGAGCACCGCGCTACGACCTGCTGCGCG | 1310 |
| Db | 1209 | gcatgcagcgaatggcgtggcctcacaagggaggagcagcgccctaggtgctgagggc | 1268 |
| QY | 1311 | CGCCCTCCGAGAACTCGCAGGAGCGCTCCGCGTGGTGCAGCACACGCGGGGAGGATGAA | 1370 |
| Db | 1269 | ggcctcagaagaactcgcaggtgcttcctcgtgtgtcagcacaggtgagcagctgaa | 1328 |
| QY | 1371 | GGGTACAGTCCGAACTGCGCGGTGCTCTCTGATCACGCTCATGTACACCATCCA | 1430 |
| Db | 1329 | ggtgtacaagtgcgaacactgcgcgtgctctcttcctgagtcacgtcatgtataccatca | 1388 |
| QY | 1431 | CATG-----GGCTGCCAGCGCTTCCGTGATCCTTTTGTGTCACATGTGCGGCTA | 1481 |
| Db | 1389 | catgggctccatggcctgcccaggtcttcggggtccctttgagtgtaacatgtgtgcta | 1448 |
| QY | 1482 | CCACAGCCAGGACCGGTAGCAGTTCCTGCTGCGACATAACGCGAGGGGAGCACCGCTTCCA | 1541 |
| Db | 1449 | tcacagccaggacaggtacagttctctatcccatatacgcgaggggagcagctgtacca | 1508 |
| QY | 1542 | CATGAGCTAA | 1551 |
| Db | 1509 | cctgagcctaa | 1518 |

